



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/729,340A
Source: FWO
Date Processed by STIC: 9/16/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/729,340A</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text .	
5 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional , please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) <input type="checkbox"/> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/729,340A

DATE: 09/16/2004

TIME: 11:25:13

Input Set : A:\PTO.LM.txt

Output Set: N:\CRF4\09162004\J729340A.raw

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Jager, Dirk
 2 Stockert, Elizabeth
 3 Scanlan, Matthew
 4 Gure, Ali
 5 Knuth, Alexander
 6 Old, Lloyd
 7 Chen, Yao-tseng
 9 <120> TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
 Antigens,
 10 the Antigens Per Se, and Uses Thereof
 12 <130> FILE REFERENCE: LUD 5793.1
 14 <140> CURRENT APPLICATION NUMBER: US 10/729,340A
 15 <141> CURRENT FILING DATE: 2003-12-04
 17 <150> PRIOR APPLICATION NUMBER: US 60/430,869
 18 <151> PRIOR FILING DATE: 2002-12-04
 20 <150> PRIOR APPLICATION NUMBER: US 10/181,663
 21 <151> PRIOR FILING DATE: 2000-11-29
 23 <150> PRIOR APPLICATION NUMBER: US 09/602,362
 24 <151> PRIOR FILING DATE: 2000-06-22
 26 <150> PRIOR APPLICATION NUMBER: US 09/451,739
 27 <151> PRIOR FILING DATE: 1999-11-30
 29 <160> NUMBER OF SEQ ID NOS: 32

ERRORED SEQUENCES

251 <210> SEQ ID NO: 8

252 <211> LENGTH: 772

253 <212> TYPE: DNA

254 <213> ORGANISM: Homo sapiens

255 <221> NAME/KEY: CDS

256 <222> LOCATION: 695,714

257 <400> SEQUENCE: 8

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 260 agcagggctc catggccaag gcgtagcggc aggcgtcccc cgcagacctc cccatcgacc 180
 261 ccagcgagcc ctctactgag gagatgatcc gctgcgacaa cgaatgcccc atcgagtggg 240
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 263 gccggggaaa gaacgatggg caaagccctt gagaagtcca gaaaaaaaaac agggcttata 360
 264 acaggtagtt tggggacatg cgtctaatag tgaggagaac aaaataagcc agtgtgttga 420
 265 ttacattgcc acctttgctg aggtgcagga agtgtaaaat gtatatattt aaagaatgtt 480
 266 gttagaggcc gggcgcggtg gctcacgcct gtaatcccag cactttggga ggccgaggcg 540
 267 gtccgatcac gaggtcagga gatcgagacc atcctggcta acacggtgaa acccgcgtctc 600
 268 tactaaaaat tcaaaaaaaaa aattagctgg gcgtgggtggc gggcgccctgt agtcccagct 660

see p. 2, too

insert <220> wherever <221>, <222>, or <223> is shown

what are these? the first 'n' is at location 689;

the second 'n' is at location 714

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/729,340A

DATE: 09/16/2004

TIME: 11:25:13

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Output Set: N:\CRF4\09162004\J729340A.raw

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 322 <211> LENGTH: 2030
 323 <212> TYPE: DNA
 324 <213> ORGANISM: Homo sapiens
 325 <221> NAME/KEY: CDS
 326 <222> LOCATION: 1628, 1752, 1758, 1769, 1789, 1873, 1908, 1915, 1933, 1970,
 327 1976, 2022
 (E)-> 328 <400> SEQUENCE: 15
 329 ctcggtgcgt taaagatggt cttctgaagg ctaactgagg aatgaaagtt tctattccaa 60
 330 ctaaagcctt agaattgatg gacatgcaaa ctttcaaagc agagcctccc gagaagccat 120
 331 ctgccttcga gcttgccatt gaaatgcaaa agtctgttcc aaataaagcc ttggaattga 180
 332 agaatgaaca aacattgaga gcagatgaga tactcccatc agaatccaaa caaaaggact 240
 333 atgaagaaag ttcttgggat tctgagagtc tctgtgagac tgtttcacag aaggatgtgt 300
 334 gtttacccaa ggctacacat caaaaagaaa tagataaaat aaatggaaaa ttagaagagt 360
 335 ctcttgataa tgatggtttt ctgaaggctc cctgcagaat gaaagtttct attccaacta 420
 336 aagccttaga attgatggac atgcaaaact tcaaagcaga gctcccgag aagccatctg 480
 337 ccttcgagcc tgccattgaa atgcaaaaagt ctgttccaaa taaagccttg gaattgaaga 540
 338 atgaacaaac attgagagca gatcagatgt tcccttcaga atcaaaacaa aagaagggtg 600
 339 aagaaaattc ttgggtttct gagagtctcc gtgagactgt ttcacagaag gatgtgtgtg 660
 340 tacccaaggc tacacatcaa aaagaaatgg ataaaataag tggaaaatta gaagattcaa 720
 341 ctagecctatc aaaaatcttg gatacagttc attcttgtga aagagcaagg gaacttcaa 780
 342 aagatcactg tgaacaacgt acaggaaaaa tggaaacaaat gaaaaagaag ttttgtgtac 840
 343 tgaaaaagaa actgtcagaa gcaaaaagaaa taaaatcaca gttagagaac caaaaagtta 900
 344 aatgggaaca agagctctgc agtgttgagat tgactttaaa ccaagaagaa gagaagagaa 960
 345 gaaatgccga tatattaat gaaaaaatta gggaagaatt aggaagaatc gaagagcagc 1020
 346 ataggaaaga gttagaagtg aaacaacaac ttgaacaggc tctcagaata caagatatag 1080
 347 aattgaagag tgtagaaagt aatttgaatc aggtttctca cactcatgaa aatgaaaatt 1140
 348 atctcttaca tgaaaattgc atgttgaaaa aggaaattgc catgctaaaa ctggaaatag 1200
 349 ccacactgaa acaccaatac caggaaaaag aaaataaata ctttgaggac attaagattt 1260
 350 taaaagaaaa gaatgctgaa cttcagatga ccttaaaact gaaagaggaa tcattaacta 1320
 351 aaagggcatc tcaatatagt gggcagctta aagttctgat agctgagaac acaatgctca 1380
 352 cttctaaatt gaaggaaaaa caagacaaag aaataactaga ggcagaaatt gaatcacacc 1440
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 357 ttggtttcag gaacatgcac aaagagacca acgtgaaaca cagtgtcaaa tgaaggaagc 1740
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 359 tctagatcag aaattatttc aactacaaag caaaaatatg tggttcaac agcaattagt 1860
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 365 <210> SEQ ID NO: 16
 366 <211> LENGTH: 512
 367 <212> TYPE: PRT
 368 <213> ORGANISM: Homo sapiens
 W--> 369 <400> SEQUENCE: 16

"N's" need to
 be
 explained
 (see item 9
 on Enr
 summary
 sheet)

N's need
 to be
 explained
 (see item 9)

P.3

RAW SEQUENCE LISTING

DATE: 09/16/2004

PATENT APPLICATION: US/10/729,340A

TIME: 11:25:13

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Output Set: N:\CRF4\09162004\J729340A.raw

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370 Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln
371 1 5 10 15
372 Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
373 20 25 30
374 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
375 35 40 45
376 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
377 50 55 60
378 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
379 65 70 75 80
380 Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu
381 85 90 95
382 Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly
383 100 105 110
384 Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala
385 115 120 125
386 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
387 130 135 140
388 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
389 145 150 155 160
390 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
391 165 170 175
392 Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp
393 180 185 190
394 Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro
395 195 200 205
396 Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu
397 210 215 220
398 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
399 225 230 235 240
400 Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys
401 245 250 255
402 Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser
403 260 265 270
404 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp
405 275 280 285
406 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu
407 290 295 300
408 Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu
409 305 310 315 320
410 Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln
411 325 330 335
412 Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu
413 340 345 350
414 Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu
415 325 355 360 365
416 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
417 370 375 380
418 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr

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E-->

← please correct

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TIME: 11:25:13

Input Set : A:\PTO.LM.txt

Output Set: N:\CRF4\09162004\J729340A.raw

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419 385          390          395          400
420 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met
421          405          410          415
422 Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr
423          420          425          430
424 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser
425          435          440          445
426 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu
427          450          455          460
428 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile
429 465          470          475          480
430 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp
431          485          490          495
432 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile
433          500          505          510

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780 <210> SEQ ID NO: 26

781 <211> LENGTH: 3673

782 <212> TYPE: DNA

783 <213> ORGANISM: Homo sapiens

784 <221> NAME/KEY: CDS

785 <222> LOCATION: 439, 473, 1789

W--> 786 <400> SEQUENCE: 26

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788 gggcgagtgc gagccggggg cgggtgctgg ggaagggtaa gcggaagcg agggcgaggg 120
789 gtaggggctg gggaagggcg agcgggaggc gcgggctctc tctagcaggg ggctgcagcc 180
790 atgaagaggc tcttagctgc cgctggcaag ggcgtgcggg gcccgagacc cccgaacccc 240
791 ttcagcgaac ggggtctacac tgagaaggac tacgggacca tctacttcgg ggatctaggg 300
792 aagatccata cagctgcctc ccggggccaa gtccagaagc tggagaagat gacagtaggg 360
793 aagaagcccg tcaacctgaa caaaagagat atgaagaaga ggactgctct acactggggc 420
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800 atttaattgag tctaaatgca cagccctcat gcttgccata tgtgaaggct catcagagat 840
801 agtcggcatg cttcttcagc aaaatgttga cgtctttgct gaagacatac atggaataac 900
802 tgcagaacgt tatgctgctg ctgctggagt taattacatt catcaacaac ttttgaaca 960
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805 aaaaacacct gacgaggctg cacgcttggt ggagggaaac tctgcaaaa ttcaatgtct 1140
806 ggggaaagca acatctggaa agtttgaaca gtcaacagaa gaaacaccta ggaaaatttt 1200
807 gaggcctaca aaagaaacat ctgagaaatt ttcattggca gcaaaagaaa gatctaggaa 1260
808 gatcacatgg gaggaaaaag aaacatctgt aaagactgaa tgcgtggcag gagtaacacc 1320
809 taataaaaact gaagtttttg aaaaaggaac atctaatatg attgcatgtc ctacaaaaga 1380
810 aacatctaca aaagcaagta caaatgtgga tgtgagttct gtagagccta tattcagtct 1440
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812 tgctaccaag attatctcta agagtgtctc acagaattat acgtgtttac ctgatgtctac 1560
813 atatcaaaaa gatatcaaaa caataaatca caaaatagaa gatcagatgt tcccatcaga 1620

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see p. 5

RAW SEQUENCE LISTING

DATE: 09/16/2004

PATENT APPLICATION: US/10/729,340A

TIME: 11:25:13

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 816 **agaagtagaa gagcttctcg agaagccatc tgccttcaag cctgccgttg aaatgcaaaa 1800**
 817 gactgttcca aataaagcct ttgaattgaa gaatgaacaa acattgagag cagctcagat 1860
 818 gttcccatca gaatccaaac aaaaggacga tgaagaaaat tcttgggatt ctgagagttc 1920
 819 ctgtgagacg gtttcacaga aggatgtgta tttacccaaa gctacacatc aaaaagaatt 1980
 820 cgatacctta agtggaaaat tagaagagtc tctgtttaa gatggtcttc tgaagcctac 2040
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 845 actgaaacat caacaccagg tgaaggaaaa taaatacttt gaggacatta agattttaca 3540
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1129 <210> SEQ ID NO: 32

1130 <211> LENGTH: 1397

1131 <212> TYPE: PRT

1132 <213> ORGANISM: Homo sapiens

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 1136 Arg Pro Ser Pro Phe Ser Gln Leu Val Tyr Thr Ser Asn Asp Ser Tyr
 1137 20 25 30
 1138 Ile Val His Ser Gly Asp Leu Arg Lys Ile His Lys Ala Ala Ser Arg
 1139 35 40 45
 1140 Gly Gln Val Arg Lys Leu Glu Lys Met Thr Lys Arg Lys Lys Thr Ile
 1141 50 55 60
 1142 Asn Leu Asn Ile Gln Asp Ala Gln Lys Arg Thr Ala Leu His Trp Ala

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DATE: 09/16/2004

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TIME: 11:25:13

Input Set : A:\PTO.LM.txt

Output Set: N:\CRF4\09162004\J729340A.raw

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1145          85          90          95
1146 Cys Gln Leu Asp Val Leu Asp Gly Glu His Arg Thr Pro Leu Met Lys
1147          100          105          110
1148 Ala Leu Gln Cys His Gln Glu Ala Cys Ala Asn Ile Leu Ile Asp Ser
1149          115          120          125
1150 Gly Ala Asp Ile Asn Leu Val Asp Val Tyr Gly Asn Thr Ala Leu His
1151          130          135          140
1152 Tyr Ala Val Tyr Ser Glu Ile Leu Ser Val Val Ala Lys Leu Leu Ser
1153 145          150          155          160
1154 His Gly Ala Val Ile Glu Val His Asn Lys Ala Ser Leu Thr Pro Leu
1155          165          170          175
1156 Leu Leu Ser Ile Thr Lys Arg Ser Glu Gln Ile Val Glu Phe Leu Leu
1157          180          185          190
1158 Ile Lys Asn Ala Asn Ala Asn Ala Val Asn Lys Tyr Lys Cys Thr Ala
1159          195          200          205
1160 Leu Met Leu Ala Val Cys His Gly Ser Ser Glu Ile Val Gly Met Leu
1161          210          215          220
1162 Leu Gln Gln Asn Val Asp Val Phe Ala Ala Asp Ile Cys Gly Val Thr
1163 225          230          235          240
1164 Ala Glu His Tyr Ala Val Thr Cys Gly Phe His His Ile His Glu Gln
1165          245          250          255
1166 Ile Met Glu Tyr Ile Arg Lys Leu Ser Lys Asn His Gln Asn Thr Asn
1167          260          265          270
1168 Pro Glu Gly Thr Ser Ala Gly Thr Pro Asp Glu Ala Ala Pro Leu Ala
1169          275          280          285
1170 Glu Arg Thr Pro Asp Thr Ala Glu Ser Leu Val Glu Lys Thr Pro Asp
1171          290          295          300
1172 Glu Ala Ala Pro Leu Val Glu Arg Thr Pro Asp Thr Ala Glu Ser Leu
1173 305          310          315          320
1174 Val Glu Lys Thr Pro Asp Glu Ala Ala Ser Leu Val Glu Gly Thr Ser
1175          325          330          335
1176 Asp Lys Ile Gln Cys Leu Glu Lys Ala Thr Ser Gly Lys Phe Glu Gln
1177          340          345          350
1178 Ser Ala Glu Glu Thr Pro Arg Glu Ile Thr Ser Pro Ala Lys Glu Thr
1179          355          360          365
1180 Ser Glu Lys Phe Thr Trp Pro Ala Lys Gly Arg Pro Arg Lys Ile Ala
1181          370          375          380
1182 Trp Glu Lys Lys Glu Asp Thr Pro Arg Glu Ile Met Ser Pro Ala Lys
1183 385          390          395          400
1184 Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys Gly Arg Pro Arg Lys
1185          405          410          415
1186 Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys Thr Gly Cys Val Ala
1187          420          425          430
1188 Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu Lys Gly Arg Ser Lys
1189          435          440          445
1190 Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr Lys Ala Ser Ala Asn
1191          450          455          460

```


RAW SEQUENCE LISTING

DATE: 09/16/2004

PATENT APPLICATION: US/10/729,340A

TIME: 11:25:13

Input Set : A:\PTO.LM.txt

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```

1192 Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu Glu Asp Glu Glu Tyr
1193 465                      470                      475                      480
1194 Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser Ala Lys Ile Gln Val
1195                      485                      490                      495
1196 Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met Glu Ile Asn Arg Glu
1197                      500                      505                      510
1198 Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe Lys Pro Ala Ile Glu
1199                      515                      520                      525
1200 Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu Leu Lys Asn Glu Gln
1201                      530                      535                      540
1202 Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu Ser Lys Gln Lys Asp
1203 545                      550                      555                      560
1204 Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser
1205                      565                      570                      575
1206 Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu Ile Asp
1207                      580                      585                      590
1208 Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asn Lys Asp Gly Leu Leu
1209                      595                      600                      605
1210 Lys Ala Thr Cys Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu
1211                      610                      615                      620
1212 Leu Lys Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Gly Lys Pro Ser
1213 625                      630                      635                      640
1214 Ala Phe Glu Pro Ala Thr Glu Met Gln Lys Ser Val Pro Asn Lys Ala
1215                      645                      650                      655
1216 Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro
1217                      660                      665                      670
1218 Ser Glu Ser Lys Glu Lys Asp Tyr Glu Glu Asn Ser Trp Asp Thr Glu
1219                      675                      680                      685
1220 Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala
1221                      690                      695                      700
1222 Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser
1223 705                      710                      715                      720
1224 Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser
1225                      725                      730                      735
1226 Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala
1227                      740                      745                      750
1228 Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln
1229                      755                      760                      765
1230 Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu
1231                      770                      775                      780
1232 Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu
1233 785                      790                      795                      800
1234 Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys
1235                      805                      810                      815
1236 Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu Ile Asp Lys Ile
1237                      820                      825                      830
1238 Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly Phe Leu Lys Ala
1239                      835                      840                      845
1240 Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met

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E--> 1241 850 855 860
 1242 Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe
 1243 865 870 870 875 880
 1244 Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu
 1245 885 890 895
 1246 Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu
 1247 900 905 910
 1248 Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu
 1249 915 920 925
 1250 Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His
 1251 930 935 940
 1252 Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser
 1253 945 950 955 960
 1254 Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu
 1255 965 970 975
 1256 Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met
 1257 980 985 990
 1258 Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu
 1259 995 1000 1005
 1260 Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu
 1261 1010 1015 1020
 1262 Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu Lys Arg Arg Asn
 1263 1025 1030 1035 1040
 1264 Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu Gly Arg Ile Glu
 1265 1045 1050 1055
 1266 Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln Leu Glu Gln Ala
 1267 1060 1065 1070
 1268 Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn
 1269 1075 1080 1085
 1270 Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn
 1271 1090 1095 1100
 1272 Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr
 1273 1105 1110 1115 1120
 1274 Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile
 1275 1125 1130 1135
 1276 Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu
 1277 1140 1145 1150
 1278 Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu
 1279 1155 1160 1165
 1280 Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu
 1281 1170 1175 1180
 1282 Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu Ser His His Pro
 1283 1185 1190 1195 1200
 1284 Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile Val Thr Ser Arg
 1285 1205 1210 1215
 1286 Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln
 1287 1220 1225 1230
 1288 Arg Lys Met Asn Val Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val
 1289 1235 1240 1245

← please correct

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1290 Leu His Gln Pro Leu Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys
 1291 1250 1255 1260
 1292 Ile Asn Leu Asn Tyr Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val
 1293 1265 1270 1275 1280
 1294 Ser Glu His Ala Gln Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys
 1295 1285 1290 1295
 1296 Glu Ala Glu His Met Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His
 1297 1300 1305 1310
 1298 Thr Glu Gln Gln Glu Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser
 1299 1315 1320 1325
 1300 Lys Asn Met Trp Leu Gln Gln Gln Leu Val His Ala His Lys Lys Ala
 1301 1330 1335 1340
 1302 Asp Asn Lys Ser Lys Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys
 1303 1345 1350 1355 1360
 1304 Met Gln His His Leu Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr
 1305 1365 1370 1375
 1306 Asn Asn His Leu Lys Asn Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala
 1307 1380 1385 1390
 1308 Glu Thr Glu Asn Ser
 1309 1395
 1310 LUD5793.1 SEQLISTING.doc 23
 1311 LUD5793.1 SEQLISTING.doc 1

delete

VERIFICATION SUMMARY

DATE: 09/16/2004

PATENT APPLICATION: US/10/729,340A

TIME: 11:25:14

Input Set : A:\PTO.LM.txt

Output Set: N:\CRF4\09162004\J729340A.raw

L:35 M:283 W: Missing Blank Line separator, <220> field identifier
L:38 M:283 W: Missing Blank Line separator, <400> field identifier
L:42 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:1 ✓
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:180
L:71 M:283 W: Missing Blank Line separator, <400> field identifier
L:98 M:283 W: Missing Blank Line separator, <400> field identifier
L:118 M:283 W: Missing Blank Line separator, <400> field identifier
L:140 M:283 W: Missing Blank Line separator, <400> field identifier
L:183 M:283 W: Missing Blank Line separator, <400> field identifier
L:218 M:283 W: Missing Blank Line separator, <400> field identifier
L:257 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8 ✓
L:257 M:283 W: Missing Blank Line separator, <400> field identifier
L:269 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:269 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:8
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:660 ✓
L:277 M:283 W: Missing Blank Line separator, <400> field identifier
L:285 M:283 W: Missing Blank Line separator, <400> field identifier
L:293 M:283 W: Missing Blank Line separator, <400> field identifier
L:301 M:283 W: Missing Blank Line separator, <400> field identifier
L:309 M:283 W: Missing Blank Line separator, <400> field identifier
L:317 M:283 W: Missing Blank Line separator, <400> field identifier
L:328 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:15 ✓
L:328 M:283 W: Missing Blank Line separator, <400> field identifier
L:356 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
L:356 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:15
L:356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1620
L:358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1740
L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1860
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1920
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1980
L:369 M:283 W: Missing Blank Line separator, <400> field identifier
L:415 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16 ✓
L:440 M:283 W: Missing Blank Line separator, <400> field identifier
L:448 M:283 W: Missing Blank Line separator, <400> field identifier
L:456 M:283 W: Missing Blank Line separator, <400> field identifier
L:501 M:283 W: Missing Blank Line separator, <400> field identifier
L:509 M:283 W: Missing Blank Line separator, <400> field identifier
L:517 M:283 W: Missing Blank Line separator, <400> field identifier
L:593 M:283 W: Missing Blank Line separator, <400> field identifier
L:768 M:283 W: Missing Blank Line separator, <400> field identifier
L:776 M:283 W: Missing Blank Line separator, <400> field identifier
L:786 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:26 ✓
L:786 M:283 W: Missing Blank Line separator, <400> field identifier
L:794 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:794 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:26
L:794 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:420
L:816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:1740
L:855 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY

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Input Set : A:\PTO.LM.txt

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L:990 M:283 W: Missing Blank Line separator, <400> field identifier
 L:998 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1006 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1021 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1133 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1243 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32